

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 3, 2003, 13:01:31 ; Search time 39.1304 Seconds  
(without alignments)  
189.563 Million cell updates/sec

Title: US-09-801-784A-1  
Perfect score: 173  
Sequence: 1 VEKNITVTASVDPITDILQADGSLPSAVALTSP 36

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Archived: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

SPREMBL\_21:  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protein:\*  
12: sp\_virus:\*  
13: sp\_verticillate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	160	92.5	167	2	09369
2	155	89.6	170	2	093V20
3	147	85.0	168	2	047123
4	138	79.8	170	2	047117
5	114	65.9	134	2	047122
6	113	65.3	191	16	09XDS3
7	112	64.7	25	2	09R514
8	108	62.4	166	2	09EXS3
9	108	62.4	170	2	09EXS2
10	108	62.4	184	2	051591
11	101	58.4	142	2	047124
12	97	56.1	133	2	047121
13	97	56.1	135	2	047120
14	59.5	34.4	169	16	092UV3
15	56.5	32.7	16	16	08X609
16	55.5	32.1	2078	16	098K31

17	54.5	31.5	1430	16	098HK1	Q98HK1 rhizobium 1
18	54	31.2	330	2	093SV9	Q93SV9 chlorobium
19	54	31.2	433	13	09DE24	Q9DE24 brachydanio
20	54	31.2	516	4	09UIV9	Q9UIV9 homo sapien
21	54	31.2	520	4	09UBG7	Q9UBG7 homo sapien
22	54	31.2	552	4	095723	Q95723 homo sapien
23	54	31.2	1186	9	080211	Q80211 methanobact
24	54	31.2	2328	6	095M19	Q95M19 erinaceus e
25	53.5	30.9	417	16	09WYU7	Q9WYU7 thermococ
26	53	30.6	740	16	08X728	Q8X728 escherichia
27	52	30.1	118	5	09WYU0	Q9WYU0 dtrosophila
28	52	30.1	498	16	097EM4	Q97EM4 clostridium
29	52	30.1	694	16	097EM5	Q97EM5 clostridium
30	52	30.1	2437	6	095MJ3	Q95MJ3 oyeccolagus
31	51.5	29.8	161	2	08VUJ2	Q8VUJ2 salmonella
32	51.5	29.8	350	17	08UJY5	Q8UJY5 pyrococcus
33	51.5	29.8	1708	16	08Y212	Q8Y212 anabaena sp
34	51	29.5	415	16	092BV8	Q92BV8 listeria in
35	51	29.5	833	12	065481	Q65481 bovine ente
36	51	29.5	1510	2	092465	Q92465 corynebacte
37	51	29.5	2358	16	09LIV8	Q9LIV8 streptomyce
38	50.5	29.2	194	16	09K809	Q9K809 bacillus ha
39	50.5	29.2	270	5	09NE74	Q9NE74 leishmania
40	50.5	29.2	417	16	098LJ7	Q98LJ7 rhizobium 1
41	50.5	29.2	580	16	08ZLF7	Q8ZLF7 salmonella
42	50.5	29.2	580	16	08Z242	Q8Z242 salmonella
43	50.5	29.2	1605	2	09X6M3	Q9X6M3 salmonella
44	50.5	29.2	3624	16	08Z411	Q8Z411 salmonella
45	50.5	29.2	5198	5	076518	Q76518 caenorhabdi

## ALIGNMENTS

RESULT 1  
ID Q9369 PRELIMINARY; PRT; 167 AA.  
AC Q9369;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE CS4 major fimbriae subunit CsaB.  
GN CsaB.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=EI1881A;  
RA Albom Z.D., Levine M.M., Galen J.E., Barry E.M.;  
RT "Isolation and characterization of ETEC CS4 fimbriae encoding genes,  
RT and their expression in Shigella flexneri 2a guinea strain CVD 1204."  
RT Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF296132; AAK97135.1; -  
SQ SEQUENCE 167 AA; 17344 MW; 94C77822A7C3A5A CRC64;

Query Match 92.5%; Score 160, DB 2; Length 167;  
Best Local Similarity 88.9%; Pred. No. 2.7e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VEKNITVTASVDPITDILQADGSLPSAVALTSP 36  
DB 24 VEKNITVTASVDPITDILQADGSLPSAVALTSP 59  
RESULT 2  
ID Q93V20 PRELIMINARY; PRT; 170 AA.  
AC Q93V20;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

```
DE Colonization factor antigen 1.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RX MEDLINE=94207144; PubMed=815840;
RA Zhang Z., Li S., Huang C.;
RT "Sequence analysis of CFA/I recombinant clone with electron microscopy.";
RL Chin. J. Biotechnol. 9:57-61(1993).
DR EMBL; S73191; AAB30543.1; -.
SQ SEQUENCE 170 AA; 17439 MW; 894347E2F43E56B4 CRC64;

Query Match      89.6%; Score 155; DB 2; Length 170;
Best Local Similarity 88.9%; Pred. No. 1.3e-13;
Matches 32; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VEKNITVTASVDPTIDLLQADGSAALPSAVALTYSPA 36
   |||||
Db 24 VEKNITVTASVDPAIDLLQADGNALPSAVKLAYSAPA 59

RESULT 3
Q47123 ID Q47123 PRELIMINARY; PRT; 168 AA.
AC Q47123;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01 DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CSUAI protein precursor (fragment).
GN CSUAI.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RX STRAIN=E7476A;
RA Gaastria W., Kusters J.G., Van Dijk L.;
RT "The major subunit gene for Csl4 fimbriae is duplicated in the CS14
fimbrial operon.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97491; CAA66122.1; -.
DR InterPro; IPR000719; Euk_pkinase.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 >168 CSUAI PROTEIN.
FT NON_TER 168 168
SQ SEQUENCE 168 AA; 17309 MW; 47760FCFF488317 CRC64;

Query Match      85.0%; Score 147; DB 2; Length 168;
Best Local Similarity 85.7%; Pred. No. 1.7e-12;
Matches 30; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VEKNITVTASVDPTIDLLQADGSAALPSAVALTYSP 35
   |||||
Db 24 VEKNITVTASVDPTIDLLQADGSAALPTAVDLTYLP 58

RESULT 4
Q47117 ID Q47117 PRELIMINARY; PRT; 170 AA.
AC Q47117;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CoTA precursor.
GN CoTA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RX STRAIN=C91F-6;
RA Proehlich B.J., Karakashian A., Sakellaris H., Scott J.R.;
RT "Genes for CS2 pili of enterotoxigenic Escherichia coli and their
interchangeability with those for CS1 pili.";
RL Infect. Immun. 63:4849-4856(1995).
DR EMBL; Z47800; CAA87761.1; -.
KW Signal.
FT SIGNAL 1 23
FT CHAIN 24 170 COTA.
SQ SEQUENCE 170 AA; 17739 MW; DDAA1053679E3674 CRC64;

Query Match      79.8%; Score 138; DB 2; Length 170;
Best Local Similarity 79.4%; Pred. No. 3.1e-11;
Matches 27; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKNTITVASVDPTIDLLQADGSAALPSAVALTYSP 35
   |||||
Db 25 EKNTITVASVDPTIDLLQADGSAALPSAVNIAYLP 58

RESULT 5
Q47122 ID Q47122 PRELIMINARY; PRT; 134 AA.
AC Q47122;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01 DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CsfA protein (fragment).
GN CsfA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RX STRAIN=9B1373;
RA Gaastria W., Kusters J.G., Van Dijk L.;
RT "The major subunit gene for Csl4 fimbriae is duplicated in the CS14
fimbrial operon.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97493; CAA66124.1; -.
DR NON_TER 1 1
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 13916 MW; 3EEFFDC5861396A4 CRC64;

Query Match      65.9%; Score 114; DB 2; Length 134;
Best Local Similarity 84.6%; Pred. No. 4.9e-08;
Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 VDTIDLLQADGSAALPSAVALTYSPA 36
   |||||
Db 1 VDTIDLLQADGSAALPSAVALTYSPA 26

RESULT 6
Q9XDS3 ID Q9XDS3 PRELIMINARY; PRT; 191 AA.
AC Q9XDS3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE TSAB protein (putative fimbrial subunit).
GN TSAB OR TCFB OR STY0346.
OS Salmonella typhi, and
OS Salmonella enterica.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601, 28901;
```

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.typhi; STRAIN=GIJF10007;  
 RA Hashimoto Y.;  
 RT "Identification of a putative fimbrial operon of *Salmonella typhi*."  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.enterica; STRAIN=RKS 3333;  
 RX MEDLINE=99348391; PubMed=10417651;  
 RA Folkesson A., Advani A., Sukupolvi S., Pfeifer J.D., Normark S.,  
 Lotfian S.;  
 RT "Multiple insertions of fimbrial operons correlate with the evolution  
 of *Salmonella* serovars responsible for human disease."  
 RL Mol. Microbiol. 33:612-622(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 SPECIES=S.typhi; STRAIN=CT18;  
 MEDLINE=21534947; PubMed=11677608;  
 Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,  
 Churcher C., Mungall K.L., Bentley S.P., Holden M.T.G., Sebahia M.,  
 Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
 Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,  
 Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
 Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 Whitehead S., Barrett B.G.;  
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*  
 enterica serovar Typhi CT18."  
 RL Nature 413:848-852(2001).  
 DR EMBL; AB029403; BAA82270.1; -;  
 DR EMBL; AJ242964; CAB51575.1; -;  
 DR EMBL; AL627266; CAD08771.1; -;  
 KM Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 191 AA; 20282 MW; F1DC03208131C7C0 CRC64;

Query Match 65.3%; Score 113; DB 16; Length 191;  
 Best Local Similarity 60.0%; Pred. No. 1e-07;  
 Matches 21; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 VEKNITVASVPTIDLLQADGSAALPSAVALTYSP 35  
 DB 44 VOKDITVTANIDSTIELLQADGSLPSTMLDMP 78  
 AC Q9RSJ4 PRELIMINARY; PRT; 25 AA.  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE Putative colonization factor O166 (Fragment).  
 OS *Escherichia coli*.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC *Escherichia*.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92363580; PubMed=1354200;  
 RA Sommerfelt H., Grewal H.M., Svennerholm A.M., Gastra W., Flood P.R.,  
 Viboud C., Bhan M.K.;  
 RT "Genetic relationship of putative colonization factor O166 to  
 colonization factor antigen I and coli surface antigen 4 of  
 enterotoxigenic *Escherichia coli*."  
 RL Infect. Immun. 60:3799-3806(1992).  
 SQ SEQUENCE 25 AA; 2570 MW; 9CDFEAC96A986A5 CRC64;

Query Match 64.7%; Score 112; DB 2; Length 25;  
 Best Local Similarity 92.0%; Pred. No. 1.3e-08;  
 Matches 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VEKNITVASVPTIDLLQADGSAAL 25

Db 1 VEKNITVASVPTIDLLQADGSAAL 25  
 |||||

RESULT 8  
 QY EXS3 PRELIMINARY; PRT; 166 AA.  
 AC Q9EXS3;  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Adhesin major subunit pilin.  
 GN CBLA.  
 OS Burkholderia cepacia (Pseudomonas cepacia).  
 OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;  
 OC Burkholderia.  
 OX NCBI\_TaxID=292;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCPB 3025;  
 RX MEDLINE=21157375; PubMed=11257549;  
 RA Richardson J., Stead D.E., Coutts R.H.A.;  
 RT "Incidence of the *CBLA* major subunit pilin gene amongst Burkholderia  
 species."  
 RT FEMS Microbiol. Lett. 196:61-66(2001).  
 RL EMBL; AJ304454; CAC18737.1; -;  
 SQ SEQUENCE 166 AA; 16971 MW; B05EC5C30F7242FF CRC64;

Query Match 62.4%; Score 108; DB 2; Length 166;  
 Best Local Similarity 57.1%; Pred. No. 4.3e-07;  
 Matches 20; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 VEKNITVASVPTIDLLQADGSAALPSAVALTYSP 35  
 DB 20 VOKDITVTANVDTTLEMLADGSAALPTTMQOYLP 54

RESULT 9  
 QY EXS2 PRELIMINARY; PRT; 170 AA.  
 AC Q9EXS2;  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Adhesin major subunit pilin.  
 GN CBLA.  
 OS Burkholderia cepacia (Pseudomonas cepacia).  
 OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;  
 OC Burkholderia.  
 OX NCBI\_TaxID=292;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BURKHOLDERIA CEPACIA COMPLEX;  
 RX MEDLINE=21157375; PubMed=11257549;  
 RA Richardson J., Stead D.E., Coutts R.H.A.;  
 RT "Incidence of the *CBLA* major subunit pilin gene amongst Burkholderia  
 species."  
 RT FEMS Microbiol. Lett. 196:61-66(2001).  
 RL EMBL; AJ304455; CAC18738.1; -;  
 SQ SEQUENCE 170 AA; 17587 MW; 940CA79122714B16 CRC64;

Query Match 62.4%; Score 108; DB 2; Length 170;  
 Best Local Similarity 54.3%; Pred. No. 4.4e-07;  
 Matches 19; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 VEKNITVASVPTIDLLQADGSAALPSAVALTYSP 35  
 DB 20 VOKDITVTANIDTVEMLADGSAALPTTMQOYLP 54

RESULT 10  
 QY EXS1 PRELIMINARY; PRT; 184 AA.

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AC Q51591;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Adhesin major subunit pilin.
DE CBIA.
OS Burkholderia cepacia (Pseudomonas cepacia).
OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
OC Burkholderia.
OX NCBI_TaxID=292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FC-7;
RX MEDLINE=95164502; PubMed=7532166;
RA Sajjan U.S., Sun L., Goldstein R., Forstner J.F.;
RT "Cable (cbi) type II pili of cystic fibrosis-associated Burkholderia
RT (Pseudomonas) cepacia: nucleotide sequence of the cblA major subunit
RT pilin gene and novel morphology of the assembled appendage fibers.";
RL J. Bacteriol. 177:1030-1038(1995).
DR EMBL; U10244; AAA69516.1; -.
SQ SEQUENCE 184 AA; 19180 MW; FE02ECE20D2760F9 CRC64;

Query Match 62.4%; Score 108; DB 2; Length 184;
Best Local Similarity 57.1%; Pred. No. 4.8e-07;
Matches 20; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Oy 1 VEKNITVTASVDPITDLQAGSALPSAVALTYSYSP 35
Db 20 VQKDIITVANVDITLLEMSADGSLPTTMQWQYLP 54

RESULT 11
O47124
ID Q47124 PRELIMINARY; PRT; 142 AA.
AC Q47124;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CSuA2 protein (Fragment).
GN CSuA2.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E7476A;
RA Gastra W., Kusters J.G., Van Dijk L.;
RT "The major subunit gene for Csi4 fimbrae is duplicated in the CS14
RT fimbrial operon.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97492; CAA66123.1; -.
DR InterPro; IPR000719; Euk_pkinase.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 142
SQ SEQUENCE 142 AA; 14498 MW; 932BF1A7989A4E7D CRC64;

Query Match 58.4%; Score 101; DB 2; Length 142;
Best Local Similarity 80.0%; Pred. No. 3.3e-06;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 11 VDPITDLQAGSALPSAVALTYSYSP 35
Db 1 VDPITDLQAGSALPTAVDLYLP 25

RESULT 12
O47121
ID Q47121 PRELIMINARY; PRT; 133 AA.
AC Q47121;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CsdA protein (Fragment).
GN CSDA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F595C;
RA Gastra W., Kusters J.G., Van Dijk L.;
RT "The major subunit gene for Csi4 fimbrae is duplicated in the CS14
RT fimbrial operon.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97494; CAA66125.1; -.
FT NON_TER 1
FT NON_TER 133
SQ SEQUENCE 133 AA; 13865 MW; 5CF679BEC86656EE CRC64;

Query Match 56.1%; Score 97; DB 2; Length 133;
Best Local Similarity 69.2%; Pred. No. 1.1e-05;
Matches 18; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Oy 11 VDPITDLQAGSALPSAVALTYSYSP 36
Db 1 VDPKLDLQAGTSLPDSIALTYSSA 26

RESULT 13
O47120
ID Q47120 PRELIMINARY; PRT; 135 AA.
AC Q47120;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CsdA protein (Fragment).
GN CSDA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E20738A;
RA Gastra W., Kusters J.G., Van Dijk L.;
RT "The major subunit gene for Csi4 fimbrae is duplicated in the CS14
RT fimbrial operon.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97495; CAA66126.1; -.
FT NON_TER 1
FT NON_TER 135
SQ SEQUENCE 135 AA; 14277 MW; 88964DB09C944B6F CRC64;

Query Match 56.1%; Score 97; DB 2; Length 135;
Best Local Similarity 69.2%; Pred. No. 1.1e-05;
Matches 18; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Oy 11 VDPITDLQAGSALPSAVALTYSYSP 36
Db 1 VDPKLDLQAGTSLPDSIALTYSSA 26

RESULT 14
O92JV3
ID Q92JV3 PRELIMINARY; PRT; 1869 AA.
AC Q92JV3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical signal peptide protein SMC03096.
GN R02997 OR SMC03096.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

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OC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN 1)  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=1021;  
 RC MEDLINE=21396507; PubMed=11481430;  
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
 Boistard P., Becker A., Boutry M., Cadieu E., Dreno S., Goux S.,  
 Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,  
 Pohl T., Portetelle D., Puhler A., Purnelle B., Ransperger U.,  
 Renard C., Thebaud P., Vandebol M., Weidner S., Gallbert F.,  
 RT "Analysis of the chromosome sequence of the legume symbiont  
 Sinorhizobium meliloti strain 1021.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).  
 DR EMBL; AF591792; CAC47576.1; -;  
 DR InterPro; IPR000425; MIP family.  
 DR PROSITE; PS00221; MIP; UNKNOWN.1.  
 DR Hypothetical protein; Complete proteome.  
 QY SEQUENCE 1869 AA; 19105 MW; 32851E6878708F9B CRC64;  
 DB 1323 ITVAGSAGPTLD-ISAALPALPALINTFAP 1352

Query Match 34.4%; Score 59.5; DB 16; Length 1869;  
 Best Local Similarity 45.2%; Pred. No. 38;  
 Matches 14; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

OY 5 ITVTASVDPTLDLQADGSAALPSAVALTSP 35  
 DB 1323 ITVAGSAGPTLD-ISAALPALPALINTFAP 1352

RESULT 15  
 OX8609 PRELIMINARY; PRT; 581 AA.  
 AC OX8609;  
 DT 01-MAR-2002 (TRENBLrel. 20, Created)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Gamma-glutamyltranspeptidase.  
 GN GGT OR Z4813 OR ECS4293.  
 OS Escherichia coli O157:H7.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OX NCBI\_TaxID=83334;  
 RN 1)  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=O157:H7 / EDL933 / ATCC 700927;  
 RC MEDLINE=21074935; PubMed=11206511;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 Rose D.U., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
 Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";  
 RL Nature 409:529-533 (2001).  
 RN 12)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / RMD 0509952;  
 RX MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,  
 RA Kohara S., Shiba T., Hattori M., Shingawa H.;  
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
 O157:H7 and genomic comparison with a laboratory strain K-12.";  
 RL DNA Res. 8:11-22 (2001).  
 DR EMBL; AE005668; AAC58553.1; -;  
 DR EMBL; AP002565; BAB37716.1; -;  
 DR InterPro; IPR000101; Gylttrnsptase.  
 DR Pfam; PF01019; G\_glu transpept. 1.  
 DR PRINTS; PRO1210; GGTTRANSPTASE.  
 DR TIGRFA; TIGR00066; g\_glu trans. 1.  
 DR PROSITE; PS00462; G\_GLU\_TRANSPEPTIDASE; 1.  
 KW Complete proteome.

SQ SEQUENCE 581 AA; 62035 MW; AF7DD96C67822AA CRC64;  
 QY SEQUENCE 581 AA; 62035 MW; AF7DD96C67822AA CRC64;  
 Query Match 32.7%; Score 56.5; DB 16; Length 581;  
 Best Local Similarity 40.0%; Pred. No. 25;  
 Matches 14; Conservative 9; Mismatches 7; Indels 5; Gaps 1;

OY 7 VTASVDPTLDLQADGSAALPSAVALTSP 36  
 DB 51 MVASVDATATGVVDILKEGNAVDAVAVGYALA 85

RESULT 16  
 OX8K31 PRELIMINARY; PRT; 2078 AA.  
 AC OX8K31;  
 DT 01-OCT-2001 (TRENBLrel. 18, Created)  
 DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE Hypothetical protein ml11661.  
 GN ML11661.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OX Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN 1)  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=MAFF303099;  
 RC MEDLINE=21082930; PubMed=11214968;  
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 Mesorhizobium loti.";  
 RL DNA Res. 7:331-338 (2000).  
 DR EMBL; AP002998; BAB48983.1; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 2078 AA; 207618 MW; BB575E48B8A59B48 CRC64;

Query Match 32.1%; Score 55.5; DB 16; Length 2078;  
 Best Local Similarity 40.6%; Pred. No. 156+02;  
 Matches 13; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

OY 4 NITVAGSAGPTLD-ISAALPALPALINTFAP 35  
 DB 908 SVTLGSAAGTLD-LAQPSPALPALANDFAP 938

RESULT 17  
 OX8HK1 PRELIMINARY; PRT; 1430 AA.  
 AC OX8HK1;  
 DT 01-OCT-2001 (TRENBLrel. 18, Created)  
 DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE WD-repeat protein, beta transducin-like.  
 GN ML2837.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OX Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN 1)  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=MAFF303099;  
 RC MEDLINE=21082930; PubMed=11214968;  
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 Mesorhizobium loti.";

```
RL DNA RES. 7:331-338(2000).
DR EMBL; AP003000; BAB49865.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 12.
DR PRINTS; PR00320; GPROTEINRPT.
DR ProDom; PD000018; WD40; 3.
DR SMART; SM00320; WD40; 13.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN 8.
DR PROSITE; PS00082; WD_REPEATS_2; 11.
DR PROSITE; PS00294; WD_REPEATS_REGION; 1.
KW Complete proteome.
SQ SEQUENCE 1430 AA; 153507 MW; 0B5032A1D2389E02 CRC64;

Query Match 31.5%; Score 54.5; DB 16; Length 1430;
Best Local Similarity 42.9%; Pred. No. 1.4e+02;
Matches 15; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

QY 1 VERMITTASVDPTIDILLOADGSLPSAVALTYSP 35
Db 1045 VDSNILLTASHDGTARLWDVDG-ALTTTLSEHYRP 1068

RESULT 18
Q93SU9
ID Q93SU9 PRELIMINARY; PRT; 330 AA.
AC Q93SU9
DT 01-DEC 2001 (TrEMBLrel. 19, Created)
DT 01-DEC 2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR 2002 (TrEMBLrel. 20, Last annotation update)
DE hcdg.
GN hcdg.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID 1097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20433268; PubMed=10976061;
RA Xiong J., Fischer W.M., Inoue K., Nakahara M., Bauer C.E.;
RT "Molecular evidence for the early evolution of photosynthesis.";
RL Science 289:1724-1730(2000).
DR EMBL; AY004137; AAG12417.1; -.
DR InterPro; IPR001092; HUH_bacic.
DR ProDom; PD000537; UbiA.
DR Pfam; PF01040; UbiA; 1.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN 1.
SQ SEQUENCE 430 AA; 35477 MW; 420256115A9DB9F8 CRC64;

Query Match 31.2%; Score 54; DB 2; Length 330;
Best Local Similarity 37.8%; Pred. No. 29;
Matches 14; Conservative 6; Mismatches 11; Indels 6; Gaps 1;

QY 2 EKNTVTASV-----DPTIDILLOADGSLPSAVALT 32
Db 230 EKNAALIASAVNDIAQIAIAILVAKGSTITATAVT 286

RESULT 19
Q9DE24
ID Q9DE24 PRELIMINARY; PRT; 433 AA.
AC Q9DE24
DT 01-MAR 2001 (TrEMBLrel. 16, Created)
DT 01-MAR 2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN 2002 (TrEMBLrel. 21, Last annotation update)
DE Forkhead transcription factor cl.2.
GN FOXL1.2.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID 7955;
RN [1]
RP SEQUENCE FROM N.A.

RL DNA RES. 7:111-116(1995);
RA Topczewska J.M., Topczewski J., Solnica-Krezel L., Hogan B.L.M.;
RT "Sequence and expression of zebrafish foxc1a and foxc1b, encoding conserved forkhead/winged helix transcription factors.";
RL Mech. Dev. 100:343-347(2001).
DR EMBL; AF219950; AAG44242.1; -.
DR HSSP; Q63245; 2HEF.
DR InterPro; IPR001766; TF_Fork_head.
DR Pfam; PF00250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS50039; FORK_HEAD_3; 1.
SQ SEQUENCE 433 AA; 47918 MW; 8941A9DBB9B817B9 CRC64;

Query Match 31.2%; Score 54; DB 13; Length 433;
Best Local Similarity 61.1%; Pred. No. 40;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 18 LQDGSALPSAVALTYSP 35
Db 273 LPASRAALPGSVSLTYSP 290

RESULT 20
Q9ULV9
ID Q9ULV9 PRELIMINARY; PRT; 516 AA.
AC Q9ULV9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Transcription factor RBP-L.
GN RBP-L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Saito T., Miyajima N.;
RT "Human mRNA for transcription factor RBP-L.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DDBB databases.
DR EMBL; AB027710; BAA87051.1; -.
DR InterPro; IPR002909; IPT_TIG.
DR Pfam; PF01833; TIG; 1.
SQ SEQUENCE 516 AA; 56594 MW; 272055B8A51C1A00 CRC64;

Query Match 31.2%; Score 54; DB 4; Length 516;
Best Local Similarity 40.7%; Pred. No. 49;
Matches 11; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 9 ASVDPTIDILLOADGSLPSAVALTYSP 35
Db 450 APITIPMSLVADGLFYSAPFTYTP 476

RESULT 21
Q9UBG7
ID Q9UBG7 PRELIMINARY; PRT; 520 AA.
AC Q9UBG7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Transcription factor RBP-L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PANCREAS;
```

RA Koyama K., Isaka S., Okamura S.;  
 RT "112-pa-";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Isaka S., Koyama K., Nakamura Y., Okamura S., Azuma C., Kimura T.;  
 RT "Human RBP-L";  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB024964; BAA88232.1; -;  
 DR EMBL; AB026048; BAA86121.1; -;  
 DR InterPro; IPR002909; IPT\_TIG.  
 DR Pfam; PF01833; TIG; 1  
 SQ SEQUENCE 520 AA; 57038 MW; BACF92459A77ACFB CRC64;

Query Match 31.2%; Score 54; DB 4; Length 520;  
 Best Local Similarity 40.7%; Pred. No. 49;  
 Matches 11; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

9 ASVDPTIDLLQADGSLPSAVALTYS 35  
 Db 454 APITIPMSLVRADGLFYPSAFSFTYTP 480

RESULT 22  
 ID 095723 PRELIMINARY; PRT; 552 AA.  
 AC 095723;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE DJ453C12.2 (recombining binding protein suppressor of hairless-like  
 DE (Drosophila)).  
 GN RBP5UHL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bridgeman A.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL021578; CAAL6521.1; -;  
 DR InterPro; IPR002909; IPT\_TIG.  
 DR Pfam; PF01833; TIG; 1  
 SQ SEQUENCE 552 AA; 60422 MW; 5E2EC4B12237AF43 CRC64;

Query Match 31.2%; Score 54; DB 4; Length 552;  
 Best Local Similarity 40.7%; Pred. No. 53;  
 Matches 11; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

9 ASVDPTIDLLQADGSLPSAVALTYS 35  
 Db 486 APITIPMSLVRADGLFYPSAFSFTYTP 512

RESULT 23  
 ID 080211 PRELIMINARY; PRT; 1186 AA.  
 AC 080211;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Tail protein.  
 OS Methanobacterium phage psiM2.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
 OX NCBI\_TaxID=77048;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=99009353; Pubmed=9791169;  
 RA Pfister P., Wasserrfallen A., Stettler R., Leisinger T.;  
 RT "Molecular analysis of Methanobacterium phage psiM2.";  
 RN Mol. Microbiol. 30:233-244(1998).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RA Pfister P., Wasserrfallen A., Stettler R., Leisinger T.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF065411; AAC27060.1; -;  
 SQ SEQUENCE 1186 AA; 132210 MW; F26FA6C4158B8F76 CRC64;

Query Match 31.2%; Score 54; DB 9; Length 1186;  
 Best Local Similarity 38.2%; Pred. No. 136+02;  
 Matches 13; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

1 VEXNITVTAASVDPTIDLLQADGSLPSAVALTYS 34  
 Db 35 VEVDITEDTVPILETIQDSLTPSDVEITIS 68

RESULT 24  
 ID 095MT9 PRELIMINARY; PRT; 2328 AA.  
 AC 095MT9;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Mannose-6-phosphate/insulin-like growth factor II receptor  
 DE (fragment).  
 GN M6P/IGF2R.  
 OS Eriaceae europaeus (Western European hedgehog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.  
 OX NCBI\_TaxID=9365;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21313641; Pubmed=11420613;  
 RA Killian J.K., Buckley T.R., Stewart N., Munday B.L., Jittle R.L.;  
 RT "Marsupials and Eutherians reunited: genetic evidence for the Theria  
 RT hypothesis of mammalian evolution."  
 RL Mamm. Genome 12:513-517(2001).  
 DR EMBL; AF339162; AAK71868.1; -;  
 DR InterPro; IPR002034; AIPM/HcIt\_synth.  
 DR InterPro; IPR000479; CIMR.  
 DR InterPro; IPR000562; FN\_Type\_II.  
 DR InterPro; IPR001150; Ptm\_Actinof.  
 DR InterPro; IPR001596; Pyrophosphatase.  
 DR Pfam; PF00878; CIMR; 13.  
 DR Pfam; PF00040; fn2; 1.  
 DR PROSITE; PS00095; FN\_Type\_II; 1.  
 DR PROSITE; PS00815; AIFM\_HOMOCIT\_SYNTH\_1; UNKNOWN\_1.  
 DR PROSITE; PS00023; FIBRONECTIN\_2; UNKNOWN\_1.  
 DR PROSITE; PS00850; GLY\_RADICAL; UNKNOWN\_1.  
 DR PROSITE; PS00387; PPASE; UNKNOWN\_1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 2328 2328  
 SQ SEQUENCE 2328 AA; 257157 MW; CB64DF66CED83911 CRC64;

Query Match 31.2%; Score 54; DB 6; Length 2328;  
 Best Local Similarity 47.8%; Pred. No. 2.8e+02;  
 Matches 11; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

11 VDPTIDLLQADGSLPSAVALTYS 33  
 Db 1533 VDQVQLVVEDGSPCPSTGLTY 1555

RESULT 25  
 ID 09WYU7 PRELIMINARY; PRT; 417 AA.  
 AC 09WYU7;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hypothetical protein TM0476.  
 GN TM0476.  
 OS Thermotoga maritima.

